

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 13:16:16 ON 14 AUG 2003

=> file medline biosis caplus
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

FILE 'MEDLINE' ENTERED AT 13:16:33 ON 14 AUG 2003

FILE 'BIOSIS' ENTERED AT 13:16:33 ON 14 AUG 2003
COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC. (R)

FILE 'CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

=> g protein-coupled receptor
L1 25886 G PROTEIN-COUPLED RECEPTOR

=> polynucleotide
L2 33502 POLYNUCLEOTIDE

=> nucleic acid
L3 351190 NUCLEIC ACID

=> l2 or l3
L4 374190 L2 OR L3

=> l1 and l4
L5 1103 L1 AND L4

=> l5 and 1970-2000/py
2 FILES SEARCHED...
L6 457 L5 AND 1970-2000/PY

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)

=> peter?/au and lind?/au
L8 1192 PETER?/AU AND LIND?/AU

=> linda?/au and wood?/au
L9 93 LINDA?/AU AND WOOD?/AU

=> luis?/au and parodi?/au
L10 2 LUIS?/AU AND PARODI?/AU

=> gabriel?/au and vogeli?/au
L11 0 GABRIEL?/AU AND VOGELI?/AU

=> l8 or l9 or l10
L12 1287 L8 OR L9 OR L10

=> l7 and l12
L13 0 L7 AND L12

=> d his

(FILE 'HOME' ENTERED AT 13:16:16 ON 14 AUG 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003

BEST AVAILABLE COPY

L1 25886 G PROTEIN-COUPLED RECEPTOR
L2 33502 POLYNUCLEOTIDE
L3 351190 NUCLEIC ACID
L4 374190 L2 OR L3
L5 1103 L1 AND L4
L6 457 L5 AND 1970-2000/PY
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)
L8 1192 PETER?/AU AND LIND?/AU
L9 93 LINDA?/AU AND WOOD?/AU
L10 2 LUIS?/AU AND PARODI?/AU
L11 0 GABRIEL?/AU AND VOGELI?/AU
L12 1287 L8 OR L9 OR L10
L13 0 L7 AND L12

=> logoff

Sequence Comparison A

US-09-884-430-3

; Sequence 3, Application US/09884430
 ; Patent No. US20020151046A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Santiago, Immaculada Silos
 ; TITLE OF INVENTION: 52871, A NOVEL HUMAN G PROTEIN COUPLED
 ; TITLE OF INVENTION: RECEPTOR AND USES THEREOF
 ; FILE REFERENCE: MNI-165
 ; CURRENT APPLICATION NUMBER: US/09/884,430
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: USSN 60/212,331
 ; **PRIOR FILING DATE: 2000-06-16**
 ; PRIOR APPLICATION NUMBER: USSN 60/269,758
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1044
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1044)

US-09-884-430-3

Alignment Scores:

Pred. No.:	1.04e-195	Length:	1044
Score:	1757.00	Matches:	337
Percent Similarity:	98.83%	Conservative:	1
Best Local Similarity:	98.54%	Mismatches:	4
Query Match:	90.80%	Indels:	0
DB:	10	Gaps:	0

US-09-750-373-25 (1-371) x US-09-884-430-3 (1-1044)

Qy	1	MetProAlaAsnPheThrGluGlySerPheAspSerSerGlyThrGlyGlnThrLeuAsp	20
Db	1	ATGCCAGCCAACCTTCACAGAGGGCAGCTTCGATTCCAGTGGGACCGGGCAGACGCTGGAT	60
Qy	21	SerSerProValAlaCysThrGluThrValThrPheThrGluValValGluGlyLysGlu	40
Db	61	TCTTCCCCAGTGGCTTGCACTGAAGCAGTGACTTTTACTGAAGTGGTGAAAGGAAAGGAA	120
Qy	41	TrpGlySerPheTyrTyrSerPheLysThrGluGlnLeuIleThrLeuTrpValLeuPhe	60
Db	121	TGGGGTTCCTTCTACTACTCCTTTAAGACTGAGCAATTGATAACTCTGTGGGTCCTCTTT	180
Qy	61	ValPheThrIleValGlyAsnSerValValLeuPheSerThrTrpArgArgLysLysLys	80
Db	181	GTTTTTACCATTGTTGGAACTCCGTTGTGCTTTTTTCCACATGGAGGAGAAAGAAGAAG	240
Qy	81	SerArgMetThrPhePheValThrGlnLeuAlaIleThrAspSerPheThrGlyLeuVal	100
Db	241	TCAAGAATGACCTTCTTTGTGACTCAGCTGGCCATCACAGATTCTTTCACAGGACTGGTC	300

Qy 101 AsnIleLeuThrAspIleIleTrpArgPheThrGlyAspPheThrAlaProAspLeuVal 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AACATCTTGACAGATATTATTTGGCGATTACCCGGAGACTTCACGGCACCTGACCTGGTT 360
 Qy 121 CysArgValValArgTyrLeuGlnValValLeuLeuTyrAlaSerThrTyrValLeuVal 140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 TGCCGAGTGGTCCGCTATTTGCAGGTTGTGCTGTGTACGCCTCTACCTACGTCCTGGTG 420
 Qy 141 SerLeuSerIleAspArgTyrHisAlaIleValTyrProMetLysPheLeuGlnGlyGlu 160
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 TCCCTCAGCATAGACAGATACCATGCCATCGTCTACCCCATGAAGTTCCCTTCAAGGAGAA 480
 Qy 161 LysGlnAlaArgValLeuIleValIleAlaTrpSerLeuSerPheLeuPheSerIlePro 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AAGCAAGCCAGGGTCCTCATTTGTGATCGCCTGGAGCCTGTCTTTTCTGTTCTCCATTCCC 540
 Qy 181 ThrLeuIleIlePheGlyLysArgThrLeuSerAsnGlyGluValGlnCysTrpAlaLeu 200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 ACCCTGATCATATTTGGGAAGAGGACACTGTCCAACGGTGAAGTGAGTGCTGGGCCCTG 600
 Qy 201 TrpProGlyAspSerTyrTrpThrProTyrMetThrIleValAlaPheLeuValTyrPhe 220
 |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 TGGCCTGACGACTCCTACTGGACCCCATACATGACCATCGTGGCCTTCCTGGTGTACTTC 660
 Qy 221 IleProLeuThrIleIleSerIleMetTyrGlyIleValIleArgThrIleTrpIleLys 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 ATCCCTCTGACAATCATCAGCATCATGTATGGCATTGTGATCCGAATATTTGGATTAAA 720
 Qy 241 SerLysThrTyrGluThrValIleSerAsnCysSerAspGlyLysLeuCysSerSerTyr 260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 721 AGGAAAACCTACGAAACAGTGATTTCCAACCTGCTCAGATGGGAAACTGTGCAGCAGCTAT 780
 Qy 261 AsnArgGlyLeuIleSerLysAlaLysIleLysAlaIleLysTyrSerIleIleIleIle 280
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 781 AACCGAGGACTCATCTCAAAGGCAAAAATCAAGGCTATCAAGTATAGCATCATCATCATT 840
 Qy 281 LeuAlaPheIleCysCysTrpSerProTyrPheLeuPheAspIleLeuAspAsnPheAsn 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 CTTGCCCTTCATCTGCTGTTGGAGTCCATACTTCCTGTTTGACATTTTGACAATTTCAAC 900
 Qy 301 LeuLeuProAspThrGlnGluArgPheTyrAlaSerValIleIleGlnAsnLeuProAla 320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 901 CTCCTTCCAGACACCCAGGAGCGTTTCTATGCCTCTGTGATCATTCAGAACCTGCCAGCA 960
 Qy 321 LeuAsnSerAlaIleAsnProProIleTyrCysValPheSerSerSerIleSerPhePro 340
 |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
 Db 961 TTGAATAGTGCCATCAACCCCTCATCTACTGTGTCTTCAGCAGCTCCATCTCTTTCCCC 1020
 Qy 341 CysArg 342
 ||||||
 Db 1021 TGCAGG 1026

Sequence Comparison B

LOCUS AI500347 414 bp mRNA linear EST 14-APR-1999
 DEFINITION tm95f03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165885
 3',
 mRNA sequence.
 ACCESSION AI500347
 VERSION AI500347.1 GI:4392329
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
 M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing
 Center
 Clone distribution: NCI-CGAP clone distribution information can
 be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1403 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 399.
 FEATURES Location/Qualifiers
 source 1. .414
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2165885"
 /clone_lib="NCI_CGAP_Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT7T3D-Pac
 (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco
 RI; 1st
 strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and
 cloned into
 the Not I and Eco RI sites of the modified pT7T3
 vector.
 Library is normalized, and was constructed by
 Bento

BASE COUNT	86 a	96 c	129 g	103 t
ORIGIN				

Qy	1206	CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTAGACCCTAGGGCAGTGCCAGTGC	1265
Db	414	CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTTGACCCTAGGGCAGTGCCAGTGC	355
Qy	1266	TAGGCTGAGCACCATCAGCTCTCCCAGGTCCTTGTCACCTGCTTGGGCACGTGCATGGAA	1325
Db	354	TAGGCTGAGCACCATCAGCTCTCCCAGGTCCTTGTCACCTGCTTGGGCACGTGCATGGAA	295
Qy	1326	CCCGAGCCAACTTCACCCACCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT	1385
Db	294	CCCGAGCCACTCACCCCCACCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT	235
Qy	1386	AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACTCCCCAGTTATTTCATGCCAG	1445
Db	234	AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACTCCCCAGTTATTTCATGCCAG	175
Qy	1446	CCAGGAAGGAAACGCCTTCCTTCCCCACCATTCCCAGCCCTCCTTCCCCTGAGCCAGCAC	1505
Db	174	CCAGGAAGGAAACGCC - TCCTTCCCCACCATTCCCAGCCCTCCTTCCCCTGAGCCAGCAC	116
Qy	1506	CTGAACCCAGTGAACACAGGCATTAGTGGTCCAGGGTCCTGGCTTGAGCCAGTGAGTAG	1565
Db	115	CTGAACCCAGTGAACACAGGCATCAGTGGTCCAGGGTCCTGGCTTGAGCCAGTGAGTAG	56
Qy	1566	ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGGTTATACATGAATATTCTCATTAC	1620
Db	55	ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGGTTATACATGAATATTCTCATTAC	1

WEST Search History

DATE: Thursday, August 14, 2003

Set Name Query
side by side

Hit Count Set Name
result set

DB=USPT; PLUR=YES; OP=AND

L12	l6 and L11	0	L12
L11	l7 or l8 or l9	42	L11
L10	gabriel.in. and vogeli.in.	0	L10
L9	luis.in. and parodi.in.	3	L9
L8	- linda.in. and wood.in.	17	L8
L7	peter.in. and lind.in.	22	L7
L6	L5 and isolated	1038	L6
L5	l1 and L4	1098	L5
L4	l2 or L3	48153	L4
L3	nucleic adj acid	46574	L3
L2	polynucleotide	17758	L2
L1	g adj protein adj coupled adj receptor	1594	L1

END OF SEARCH HISTORY